

## SEQUENCE LISTING

<110> DYAX CORP.

<120> MUCIN-1 Specific Binding Members and Methods of Use Thereof

<130> DYX-015.1 US, DYX-015.1 PCT

<140> not yet assigned

<141> 2001-03-30

<150> US 09/538,913

<151> 2000-03-30

<160> 112

<170> PatentIn version 3.0

<210> 1

<211> 113

<212> PRT

<213> synthetic

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1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser  
20 25 30

Asn Gly Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser  
35 40 45

Pro Gln Leu Leu Ile Tyr Ser Gly Ser His Arg Ala Ser Gly Val Pro  
50 55 60

Asp Arg Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Arg Ile  
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly  
85 90 95

Leu Gln Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys  
100 105 110

Arg

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 tacctgcaga agccagggca gtctccacag ctctgatct attcgggttc tcatcggggc 180  
 tccgggggtcc ctgacagggt cagtggcagt gtatcaggca cagattttac actgagaatc 240  
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 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Asn  
 20 25 30  
 Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly

100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser  
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ccaggaagg ggctggagtg ggtctcaggt attagtggta gtggtggcag cacatactac 180  
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240  
ctgcaaataga acagcctgag agccgaggac acggccgtat attattgtgc gaaacatacc 300  
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agc 363

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20 25 30  
Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly  
 100 105 110  
 Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ala Leu Glu Ile  
 115 120 125  
 Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro  
 130 135 140  
 Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly  
 145 150 155 160  
 Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln  
 165 170 175  
 Leu Leu Ile Tyr Ser Gly Ser His Arg Ala Ser Gly Val Pro Asp Arg  
 180 185 190  
 Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Arg Ile Ser Arg  
 195 200 205  
 Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Leu Gln  
 210 215 220  
 Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Gly  
 225 230 235 240  
 Gly Gly Ser Gly Gly Gly Ala Leu Ala Pro Thr Ser Ser Ser Thr Lys  
 245 250 255  
 Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile  
 260 265 270  
 Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu  
 275 280 285  
 Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu  
 290 295 300  
 Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu  
 305 310 315 320  
 Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn

	325		330		335	
Ile Asn Val	Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met					
340		345		350		
Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg						
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 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240  
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 cagggcttac agagtccatt cactttcggc cctgggacca aagtggatat caaacgaggg 720  
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 aatcccaaac tcaccaggat gctcacattt aagttttaca tgcccaagaa ggccacagaa 900

ctgaaacatc ttcagtgtct agaagaagaa ctcaaacctc tggaggaagt gctaaattta 960  
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gttctggaac taaagggatc tgaaacaaca ttcatgtgtg aatatgctga tgagacagca 1080  
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act 1143

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<212> PRT  
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<400> 7

Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly  
1 5 10 15

Ser Thr Ala Pro  
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<210> 8  
<211> 20  
<212> PRT  
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<400> 8

Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro  
1 5 10 15

Pro Ala His Gly  
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<210> 9  
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<400> 9

gtccttgacc aggcagccca gggc

24

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<211> 23  
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<400> 10  
 agcggataac aatttcacac agg 23

<210> 11  
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<210> 16  
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 <212> DNA  
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69

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<400> 18

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 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60



Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys

<210> 19  
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<400> 19

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly  
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser  
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser  
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro  
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile  
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala  
85 90 95

Leu Gln Thr Pro  
100

<210> 20  
<211> 14  
<212> PRT  
<213> synthetic

<400> 20

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala  
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<210> 21  
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 <212> DNA  
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<400> 21  
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42

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 <211> 6  
 <212> PRT  
 <213> synthetic

<400> 22

His His His His His His  
 1 5

<210> 23  
 <211> 18  
 <212> DNA  
 <213> synthetic

<400> 23  
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18

<210> 24  
 <211> 220  
 <212> PRT  
 <213> synthetic

<400> 24

Glu Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly  
 1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser  
 20 25 30

Asn Gly Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser  
 35 40 45

Pro Gln Leu Leu Ile Tyr Ser Gly Ser His Arg Ala Ser Gly Val Pro  
 50 55 60

Asp Arg Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Arg Ile  
 65 70 75 80  
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly  
 85 90 95  
 Leu Gln Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys  
 100 105 110  
 Arg Gly Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 115 120 125  
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
 130 135 140  
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
 145 150 155 160  
 Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
 165 170 175  
 Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
 180 185 190  
 Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
 195 200 205  
 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 210 215 220

<210> 25  
 <211> 663  
 <212> DNA  
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 tccgggggtcc ctgacagggt cagtggcagt gtatcaggca cagattttac actgagaatc 240  
 agcagagtgg aggctgagga tggttgagtt tattactgca tgcagggtct acagagtcca 300  
 ttcactttcg gccctgggac caaagtggat atcaaacgag gaactgtggc tgcaccatct 360

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gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc      420
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgcctc      480
caatcgggta actcccagga gagtgtcaca gacgaggaca gcaaggacag cacctacagc      540
ctcagcagca ccttgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc      600
gaagtcaccc atcagggcct gagttcaccc gtagacaaaga gcttcaacag gggagagtgt      660
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<213> synthetic

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<400> 26

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20              25              30
Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35              40              45
Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50              55              60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65              70              75              80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85              90              95
Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly
100             105             110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115             120             125
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130             135             140

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Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

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tctgtgcag	cctctggatt	cacgtttaga	agtaacgcca	tgggctgggt	cgcagggt		120
ccaggaagg	ggctggagt	ggtctcaggt	attagtggta	gtggtggcag	cacatactac		180
gcagactccg	tgaagggccg	gttcaccatc	tccagagaca	attccaagaa	cacgtgtat		240
ctgcaaata	acagcctgag	agccgaggac	acggccgtat	attattgtgc	gaaacatacc		300
ggggggggcg	tttgggaccc	cattgactac	tggggccagg	gaaccctggg	caccgtctca		360
agcgcccca	ccaagggcc	atcggtcttc	cccctggcac	cctcctccaa	gagcacctct		420
gggggcacag	cgccctggg	ctgcctggtc	aaggactact	tccccgaacc	ggtgacggtg		480
tcgtggaact	caggcgccct	gaccagcggc	gtccacacct	tccggctgt	cctacagtcc		540
tcaggactct	actccctcag	cagcgtagtg	accgtgccct	ccagcagctt	gggcacccag		600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaagttgag		660
cccaaattct	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg		720
ggaccgtcag	tcttctctct	cccccaaaa	ccaaggaca	ccctcatgat	ctcccgacc		780
cctgaggtca	catgcgtggg	ggtggacgtg	agccacgaag	accctgaggt	caaattcaac		840

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aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc     1020
tccaaagcca aagggcagcc ccgagaacca caggtgtaca cctgcccc atcccgggat     1080
gagctgacca agaaccaggt cagcctgacc tgcttggtca aaggcttcta tcccagcgac     1140
atgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc     1200
gtgctggact ccgacggctc cttcttctc tacagcaagc tcaccgtgga caagagcagg     1260
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<210> 28
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<220>
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<222> (1)..(14)
<223> Xaa is varied according to the disclosure

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<400> 28

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Xaa Xaa His Thr Gly Xaa Gly Val Trp Xaa Pro Xaa Xaa Xaa
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<210> 29
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<400> 29

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Ala Lys His Thr Gly Arg Gly Val Trp Asp Pro Ile Gly Tyr
1           5           10

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<210> 30

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<400> 30

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Lys His  
 1 5 10

<210> 31  
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<400> 31

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr  
 1 5 10

<210> 32  
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<400> 32

Ala Ile His Thr Gly Gly Gly Val Trp Asp Pro Ile Lys Tyr  
 1 5 10

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<220>  
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 <223> n is varied according to the disclosure

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 <211> 39  
 <212> DNA



<213> synthetic

<220>

<221> primer

<222> (1)..(39)

<223> n is varied according to the disclosure

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39

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<211> 90

<212> DNA

<213> synthetic

<220>

<221> primer

<222> (1)..(90)

<223> n is varied according to the disclosure

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nnnnnnnnnn nnnnnnacaat aatatacggc

90

<210> 36

<211> 90

<212> DNA

<213> synthetic

<220>

<221> primer

<222> (1)..(90)

<223> n=a,c,g, or t

<400> 36

ctatgagacg gtgaccaggg ttccttgccc ccagtagtca atgggggtccc aaacmnnmnn

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mnnmnnmnnnt ttcgcacaat aatatacggc

90

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 <223> n=a,c,g, or t

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<210> 38  
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<210> 39  
 <211> 56  
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<400> 39  
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Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala Leu  
 1 5 10 15

<210> 41  
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<400> 41

Ala	Lys	His	Asn	Thr	Ser	Lys	Val	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
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<210> 42

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<212> DNA

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<212> PRT

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Ala	Lys	Ser	Ser	Thr	Thr	Thr	Val	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 44

<211> 48

<212> DNA

<213> synthetic

<400> 44

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48

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<211> 16

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<221> PEPTIDE

<222> (1)..(16)

<223> Xaa is varied according to the disclosure

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1 5 10 15

<210> 46  
<211> 48  
<212> DNA  
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<400> 46  
gcgaaatagc ctatggcgaa tgtttgggac cccattgact actggggc

48

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<220>  
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<222> (1)..(16)  
<223> Xaa is varied according to the disclosure

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Ala Lys Xaa His Thr Lys Thr Val Trp Asp Pro Ile Asp Tyr Trp Gly  
1 5 10 15

<210> 48  
<211> 48  
<212> DNA  
<213> synthetic

<400> 48  
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48

<210> 49  
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<212> PRT  
<213> synthetic

<400> 49

Tyr Trp Gly  
1

<210> 50  
 <211> 48  
 <212> DNA  
 <213> synthetic

<400> 50

gcgaaaatta ctgtagtcg tgtttgggac cccattgact actggggc

48

<210> 51  
 <211> 16  
 <212> PRT  
 <213> synthetic

<400> 51

Ala	Lys	Arg	Tyr	Leu	Tyr	Asp	Val	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 52  
 <211> 48  
 <212> DNA  
 <213> synthetic

<400> 52

gcgaaacggt atctgtatga tgtttgggac cccattgact actggggc

48

<210> 53  
 <211> 16  
 <212> PRT  
 <213> synthetic

<400> 53

Ala	Lys	His	Thr	Gly	Gly	Gly	Thr	Leu	Gln	Arg	Leu	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 54  
 <211> 48  
 <212> DNA  
 <213> synthetic

<400> 54

gcgaaacata ccgggggggg cactttgcag cggctggact actggggc

48

<210> 55  
 <211> 16  
 <212> PRT  
 <213> synthetic

<400> 55

Ala	Lys	His	Thr	Gly	Gly	Gly	Thr	Gln	Thr	Pro	Cys	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 56  
 <211> 48  
 <212> DNA  
 <213> synthetic

<400> 56

gcgaaacata ccgggggggg cactcagact ccgtgtgact actggggc

48

<210> 57  
 <211> 16  
 <212> PRT  
 <213> synthetic

<400> 57

Ala	Lys	His	Thr	Gly	Gly	Gly	Arg	Arg	Ile	Cys	His	Asp	Tyr	Trp	Gly
1				5					10					15	

<210> 58  
 <211> 48  
 <212> DNA  
 <213> synthetic

<400> 58

gcgaaacata ccgggggggg ccgtcgtatt tgtcatgact actggggc

48

<210> 59  
 <211> 16  
 <212> PRT  
 <213> synthetic

<220>

<221> PEPTIDE

<222> (1) .. (16)

<223> Xaa is varied according to the disclosure

<400> 59

Ala	Lys	His	Thr	Gly	Gly	Gly	Xaa	Arg	Xaa	Xaa	Arg	Asp	Tyr	Trp	Gly
1				5					10					15	

<210> 60

<211> 48

<212> DNA

<213> synthetic

<400> 60

gcgaaacata ccggggggggg ctagcggttag tagcgggact actggggc

48

<210> 61

<211> 16

<212> PRT

<213> synthetic

<400> 61

Ala	Lys	His	Thr	Gly	Gly	Gly	Gln	Lys	Leu	Gln	Leu	Asp	Tyr	Trp	Gly
1				5					10					15	

<210> 62

<211> 48

<212> DNA

<213> synthetic

<400> 62

gcgaaacata ccggggggggg ccagaagctg cagctggact actggggc

48

<210> 63

<211> 16

<212> PRT

<213> synthetic

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa may be varied according to the disclosure to form alternate peptide

&lt;400&gt; 63

Ala	Xaa	His	Thr	Gly	Gly	Arg	Gly	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
1				5				10						15	

&lt;210&gt; 64

&lt;211&gt; 48

&lt;212&gt; DNA

&lt;213&gt; synthetic

&lt;400&gt; 64

gcgtsacata cggggggggcg cggttgggac cccattgact actggggc

48

&lt;210&gt; 65

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; synthetic

&lt;400&gt; 65

Ala	Asn	Gln	Thr	Gly	Gly	Gly	Val	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
1				5				10						15	

&lt;210&gt; 66

&lt;211&gt; 48

&lt;212&gt; DNA

&lt;213&gt; synthetic

&lt;400&gt; 66

gcgaaccaga ctggggggggg cgtttgggac cccattgact actggggc

48

&lt;210&gt; 67

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; synthetic

&lt;400&gt; 67

Ala	Arg	His	Thr	Gly	Gly	Gly	Val	Trp	Asp	Pro	Ile	Tyr	Tyr	Trp	Gly
1				5				10						15	

&lt;210&gt; 68

&lt;211&gt; 48

&lt;212&gt; DNA



<213> synthetic

<400> 68

gcgagacata ccggtggggg cgtktgggat cccatatact actggggc

48

<210> 69

<211> 16

<212> PRT

<213> synthetic

<400> 69

Ala	Lys	Pro	Thr	Gly	Gly	Gly	Ala	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 70

<211> 48

<212> DNA

<213> synthetic

<400> 70

gcgaaaccta ccgggggggg cgcttgggac cccattgact actggggc

48

<210> 71

<211> 16

<212> PRT

<213> synthetic

<400> 71

Ala	Lys	His	Thr	Gly	Val	Gly	Val	Trp	His	Pro	Ile	Tyr	Tyr	Trp	Gly
1				5				10						15	

<210> 72

<211> 48

<212> DNA

<213> synthetic

<400> 72

gcgaaacata ccggggtggg cgtttggcac cccatctact actggggc

48

<210> 73

<211> 14

<212> PRT

<213> synthetic

<400> 73

Ala Lys His Thr Gly Val Gly Val Trp Asp Pro Ile Lys Tyr  
1 5 10

<210> 74

<211> 14

<212> PRT

<213> synthetic

<400> 74

Ala Lys His Thr Gly Glu Gly Val Trp Asp Pro Ile Lys Tyr  
1 5 10

<210> 75

<211> 14

<212> PRT

<213> synthetic

<400> 75

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Lys  
1 5 10

<210> 76

<211> 14

<212> PRT

<213> synthetic

<400> 76

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr  
1 5 10

<210> 77

<211> 14

<212> PRT

<213> synthetic

<400> 77

Ala Arg His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr  
1 5 10

<210> 78  
 <211> 14  
 <212> PRT  
 <213> synthetic

<400> 78

Ser Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr  
 1 5 10

<210> 79  
 <211> 14  
 <212> PRT  
 <213> synthetic

<400> 79

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly His  
 1 5 10

<210> 80  
 <211> 14  
 <212> PRT  
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<400> 80

Ala Lys His Thr Gly Gly Gly Val Trp Asn Pro Ile Gly His  
 1 5 10

<210> 81  
 <211> 14  
 <212> PRT  
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<400> 81

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Leu Gly Tyr  
 1 5 10

<210> 82  
 <211> 14  
 <212> PRT  
 <213> synthetic

<400> 82

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Leu Asp Asn  
 1 5 10

<210> 83  
 <211> 14  
 <212> PRT  
 <213> synthetic

<400> 83

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Tyr  
 1 5 10

<210> 84  
 <211> 14  
 <212> PRT  
 <213> synthetic

<400> 84

Ala Arg His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Tyr  
 1 5 10

<210> 85  
 <211> 14  
 <212> PRT  
 <213> synthetic

<400> 85

Ala Lys His Thr Gly Ser Gly Val Trp Asp Pro Ile Asn Tyr  
 1 5 10

<210> 86  
 <211> 14  
 <212> PRT  
 <213> synthetic

<400> 86

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Asp  
 1 5 10

<210> 87  
 <211> 14  
 <212> PRT  
 <213> synthetic

&lt;400&gt; 87

Ala Lys His Thr Gly Val Gly Val Trp Asp Pro Met Asn Tyr  
 1 5 10

&lt;210&gt; 88

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; synthetic

&lt;400&gt; 88

Thr Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Tyr  
 1 5 10

&lt;210&gt; 89

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; synthetic

&lt;400&gt; 89

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ala Tyr  
 1 5 10

&lt;210&gt; 90

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; synthetic

&lt;400&gt; 90

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ala Asn  
 1 5 10

&lt;210&gt; 91

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; synthetic

&lt;400&gt; 91

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Phe Ala Tyr  
 1 5 10

&lt;210&gt; 92

<211> 14  
 <212> PRT  
 <213> synthetic

<400> 92

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Met Ala Ser  
 1 5 10

<210> 93  
 <211> 14  
 <212> PRT  
 <213> synthetic

<400> 93

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Met Asp Tyr  
 1 5 10

<210> 94  
 <211> 14  
 <212> PRT  
 <213> synthetic

<400> 94

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile His Tyr  
 1 5 10

<210> 95  
 <211> 14  
 <212> PRT  
 <213> synthetic

<400> 95

Ala Ile His Thr Gly Ala Gly Val Trp Asp Pro Ile Arg Tyr  
 1 5 10

<210> 96  
 <211> 14  
 <212> PRT  
 <213> synthetic

<400> 96

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ser Ser

1 5 10

<210> 97  
 <211> 14  
 <212> PRT  
 <213> synthetic

<400> 97

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Asp  
 1 5 10

<210> 98  
 <211> 14  
 <212> PRT  
 <213> synthetic

<400> 98

Val Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Val Tyr  
 1 5 10

<210> 99  
 <211> 14  
 <212> PRT  
 <213> synthetic

<400> 99

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Val Asp Tyr  
 1 5 10

<210> 100  
 <211> 14  
 <212> PRT  
 <213> synthetic

<400> 100

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Val Pro  
 1 5 10

<210> 101  
 <211> 14  
 <212> PRT  
 <213> synthetic

<400> 101

Val Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ala Tyr  
1 5 10

<210> 102

<211> 14

<212> PRT

<213> synthetic

<400> 102

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile His Asn  
1 5 10

<210> 103

<211> 14

<212> PRT

<213> synthetic

<400> 103

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Met His Tyr  
1 5 10

<210> 104

<211> 14

<212> PRT

<213> synthetic

<400> 104

Ala Lys His Thr Gly Gly Gly Val Trp Asn Pro Ile Asp Tyr  
1 5 10

<210> 105

<211> 14

<212> PRT

<213> synthetic

<400> 105

Val Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr  
1 5 10

<210> 106

<211> 14



<212> PRT  
 <213> synthetic

<400> 106

Ala Lys His Thr Gly Ala Gly Val Trp Asp Pro Ile Asp Tyr  
 1 5 10

<210> 107  
 <211> 14  
 <212> PRT  
 <213> synthetic

<400> 107

Ala Gln His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr  
 1 5 10

<210> 108  
 <211> 14  
 <212> PRT  
 <213> synthetic

<400> 108

Ala Lys His Thr Gly Arg Gly Val Trp Asp Pro Ile Asp Tyr  
 1 5 10

<210> 109  
 <211> 14  
 <212> PRT  
 <213> synthetic

<400> 109

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Tyr Tyr  
 1 5 10

<210> 110  
 <211> 66  
 <212> DNA  
 <213> synthetic

<400> 110  
 ggactagtcc tggagtgcgc gcactcccag gtccagctgg tgcagtctgg gggaggcttg 60  
 gtacag 66

<210> 111  
<211> 73  
<212> DNA  
<213> synthetic

<400> 111  
gcgctcgcat ttgctgtta attaagttag atctattcta ctcacgtttg atatccactt 60  
tggtcccagg gcc 73

<210> 112  
<211> 35  
<212> DNA  
<213> synthetic

<400> 112  
ccagtgcact ccgaaattgt gctgactcag tctcc 35